The following Listing of the Claims will replace all prior versions and all prior listings of the claims in the present application:

1.-16. (Cancelled)

17. (Currently amended) A method of identifying two or more markers useful for diagnosing a disease, said method comprising:

for each gene of a collection of two or more genes, wherein said gene is expressed in blood and in a non-blood tissue of a subject not having said disease:

(a) using an oligonucleotide of predetermined sequence, detecting a presence, in RNA of blood samples which have not been fractionated into cell types from subjects having said disease, of RNA encoded by said gene, said oligonucleotide being specific only for RNA, and/or cDNA complementary to said RNA, encoded by said gene in said samples;

(b) quantifying a level of said RNA encoded by said gene; and

(c) determining a difference between said level, and a quantified level of control RNA encoded by said gene in RNA of blood samples which have not been fractionated into cell types from control subjects, said control RNA having been detected in said samples from said control subjects, and said difference identifying said gene as a marker of said disease,

thereby identifying said two or more markers useful for diagnosing said disease.

18. (Cancelled)

19. (Currently amended) A method of identifying two or more markers useful for diagnosing a disease, said method comprising:

for each gene of a collection of two or more genes, wherein said gene is expressed in blood and in a non-blood tissue of a subject not having said disease:

(a) producing amplification products from RNA of blood samples which have not been fractionated into cell types from subjects having said disease, using primers specific only for RNA, and/or cDNA complementary to said RNA, encoded by said gene in said sample;

(b) quantifying a level of said amplification products; and

(c) determining a difference between said level of said amplification products, and a quantified level of control amplification products produced from control RNA using primers

specific only for said RNA, and/or cDNA complementary to said RNA, encoded by said gene in RNA of blood samples which have not been fractionated into cell types from control subjects, said control ~~amplification products~~RNA having been detected in said samples from said control subjects, wherein said difference identifies said gene as a marker of said disease,

thereby identifying said two or more markers useful for diagnosing said disease.

20. (Currently amended) The method of any one of claims 17 and ~~54~~57, wherein said detecting of said RNA encoded by said gene of step (a) is effected by detecting cDNA and/or EST derived from said RNA encoded by said gene of step (a).

21. (Currently amended) The method of any one of claims 19 and ~~55~~58, wherein said producing of said amplification products of step (a) is effected by producing amplification products from cDNA and/or EST derived from said RNA encoded by said gene of step (a).

22. (Cancelled)

23. (Currently amended) The method of any one of claims 17 and ~~54~~57, further comprising quantifying said control RNA to determine said quantified level of said control RNA.

24. (Currently amended) The method of any one of claims 19 and ~~55~~58, further comprising quantifying a level of said control amplification products to thereby determine said quantified level of said control amplification products.

25–27. (Cancelled)

28. (Currently amended) The method of any one of claims 17 and ~~54~~57, wherein said quantifying of said level of said RNA encoded by said gene ~~in~~ of step (b) is effected by determining a quantity of said RNA encoded by said gene of step (a) relative to a housekeeping gene.

29 (Currently amended) The method of any one of claims 17 and ~~54~~57, wherein said quantified level of said control RNA encoded by said gene has been determined relative to a

housekeeping gene.

30. (Cancelled)

31. (Currently amended) The method of any one of claims 19 and ~~55~~58, wherein said quantified level of said amplification products produced from said control RNA has been determined relative to a housekeeping gene.

32. (Cancelled)

33. (Currently amended) The method of any one of claims 17, 19, ~~54~~–57 and ~~55~~58, wherein said control subjects and said subjects having said disease are human.

34. (Currently amended) -The method of any one of claims 17, 19, ~~54~~–57 and ~~55~~58, wherein said control subjects do not have said disease.

35–37. (Cancelled)

38. (Currently amended) The method of any one of claims 19 and ~~55~~58, wherein said quantifying of said amplification products encoded by said gene ~~in~~ of step (b) is effected by quantifying amplification products produced from cDNA and/or EST derived from said RNA encoded by said gene of step (a).

39–40. (Cancelled)

41. (Currently amended) The method of any one of claims 17 and ~~54~~57, wherein said quantifying of said level of said RNA encoded by said gene ~~in~~ of step (b) is effected by quantifying a level of cDNA and/or EST derived from said RNA encoded by said gene of step (a).

42. (Cancelled)

43. (Currently amended) The method of any one of claims 17, 19, ~~54~~ 57 and ~~55~~58, wherein said disease is ~~selected from the group consisting of~~ colorectal cancer~~, diabetes, and heart failure~~.

44–48. (Cancelled)

49. (Currently amended) The method of any one of claims 17, 19, ~~54~~ 57 and ~~55~~58, wherein said control subjects have said disease at a different stage than said subjects having said disease.

50–55. (Cancelled)

56. (Currently amended) The method of any one of claims 19 ~~or~~and ~~55~~58, wherein said quantifying of said level of said amplification products encoded by said gene ~~in~~ of step (b) is effected by determining a quantity of said amplification products relative to a housekeeping gene.

57. (New) A method of identifying two or more markers useful for diagnosing a disease, said method comprising:

for each gene of a collection of two or more genes, wherein said gene is expressed in blood and in a non-blood tissue of a subject not having said disease:

(a) using an oligonucleotide of predetermined sequence, detecting a presence, in RNA of blood samples which comprise leukocytes which have not been fractionated into cell types from subjects having said disease, of RNA encoded by said gene, said oligonucleotide being specific only for RNA, and/or cDNA complementary to said RNA, encoded by said gene in said samples;

(b) quantifying a level of said RNA encoded by said gene; and

(c) determining a difference between said level, and a quantified level of control RNA encoded by said gene in RNA of blood samples which comprise leukocytes which have not been fractionated into cell types from control subjects, said control RNA having been detected in said samples from said control subjects, and said difference identifying said gene as a marker of said disease,

thereby identifying said two or more markers useful for diagnosing said disease.

58. (New) A method of identifying two or more markers useful for diagnosing a disease, said method comprising:

for each gene of a collection of two or more genes, wherein said gene is expressed in blood and in a non-blood tissue of a subject not having said disease:

(a) producing amplification products from RNA of blood samples which comprise leukocytes which have not been fractionated into cell types from subjects having said disease, using primers specific only for RNA, and/or cDNA complementary to said RNA, encoded by said gene in said sample;

(b) quantifying a level of said amplification products; and

(c) determining a difference between said level of said amplification products, and a quantified level of control amplification products produced from control RNA using primers specific only for said RNA, and/or cDNA complementary to said RNA, encoded by said gene in RNA of blood samples which comprise leukocytes which have not been fractionated into cell types from control subjects, said control RNA having been detected in said samples from said control subjects, wherein said difference identifies said gene as a marker of said disease,

thereby identifying said two or more markers useful for diagnosing said disease.

59. (New) The method of any one of claims 17, 19, 57 and 58, wherein said disease is diabetes.

60. (New) The method of any one of claims 17, 19, 57 and 58, wherein said disease is heart failure.

61. (New) The method of any one of claims 17, 19, 57 and 58, wherein said gene is predominantly expressed in said non-blood tissue.